
Single-cell resolution of morphological changes in hemogenic endothelium.

Journal: Development

Publication Year: 2015

Authors: Frank L Bos, John S Hawkins, Ann C Zovein

PubMed link: 26243871

Funding Grants: Human endothelial reprogramming for hematopoietic stem cell therapy.

Public Summary:

To understand the cellular events that generate the first hematopoietic stem cells in the embryo, we correlate cell surface changes with protein expression, using state of the art microscopy techniques. We are able to identify early changes in the cell transition from an endothelial cell to a hematopoietic cell, and provide a new technical resource that is widely applicable for analyses of single cells in their native tissue environments.

Scientific Abstract:

Endothelial-to-hematopoietic transition (EHT) occurs within a population of hemogenic endothelial cells during embryogenesis, and leads to the formation of the adult hematopoietic system. Currently, the prospective identification of specific endothelial cells that will undergo EHT, and the cellular events enabling this transition, are not known. We set out to define precisely the morphological events of EHT, and to correlate cellular morphology with the expression of the transcription factors RUNX1 and SOX17. A novel strategy was developed to allow for correlation of immunofluorescence data with the ultrastructural resolution of scanning electron microscopy. The approach can identify single endothelial cells undergoing EHT, as identified by the ratio of RUNX1 to SOX17 immunofluorescence levels, and the morphological changes associated with the transition. Furthermore, this work details a new technical resource that is widely applicable for correlative analyses of single cells in their native tissue environments.

Source URL: <https://www.cirm.ca.gov/about-cirm/publications/single-cell-resolution-morphological-changes-hemogenic-endothelium>